

IN THE SPECIFICATION:

Please amend the Specification as follows:

Page 5, lines 13-14, please replace the paragraph as follows:

Figure 1 shows the degree of identity between the predicted amino acid sequence of the human NPY-Y1 (**hy1p; SEQ ID NO: 6**), NPY-Y2 (**hy2p; SEQ ID NO: 7**) and NPY-Y7 receptors (**hy7p; SEQ ID NO: 2**).

Page 5, lines 24-25, please replace the paragraph as follows:

Figure 4 shows the degree of identity between the predicted amino acid sequence of the human **NPY-Y7 receptor (hy7; SEQ ID NO: 2)** and murine NPY-Y7 receptors (**mY7; SEQ ID NO: 3**).

Page 6, lines 22-34, please replace the paragraph as follows:

Screening of a medium resolution Stanford G3 panel of 83 clones was performed to further refine the map position of the hy7 gene. PCR amplification was carried out on this panel using primers hy7-A (5'GGATGGCCATTTGGAAAC3'; **SEQ ID NO: 8**) and hy7-B (5'CCAATCCTTCCATACATG3'; **SEQ ID NO: 9**), corresponding to nucleotides 507-524 and 890-907 of the hy7 cDNA (SEQ ID NO: 4), respectively. The analysis indicated that the hy7 gene is most closely associated with the marker SHGC-418 on the long arm of chromosome 4. This map location is defined by markers AFM191xh2 and AFM347ZH1. Assessment of the flanking markers using the Whitehead/MIT STS-Based Map of the Human Genome)(http://www-genome.wi.mit.edu/cgi-bin/contig/phys_map)

in conjunction with The Genome Directory (Adams, M.D., et al. Nature 377 Suppl. (1995)) identifies 4q21.3 as the most likely position of the hy7 gene.